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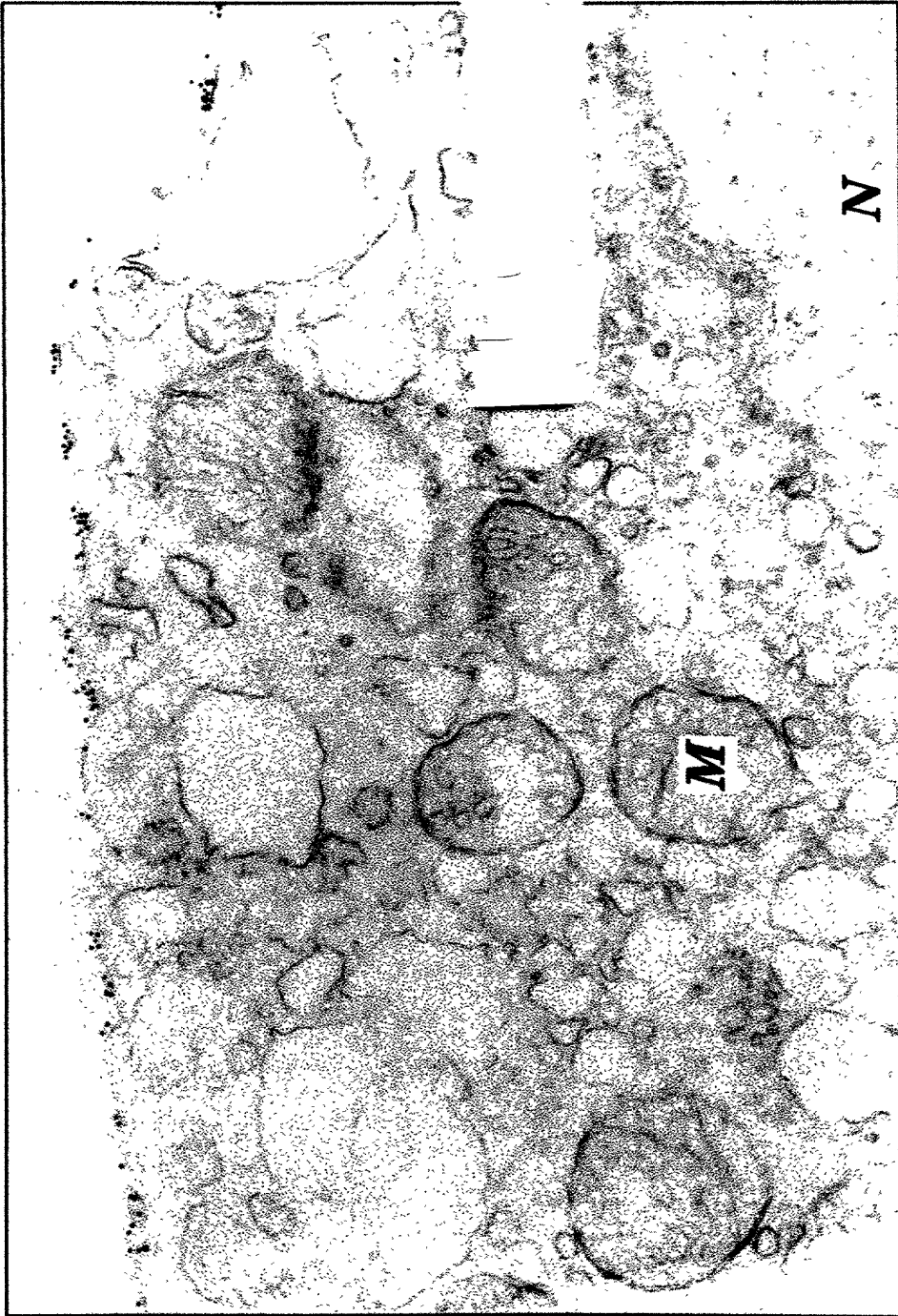


FIG. 1

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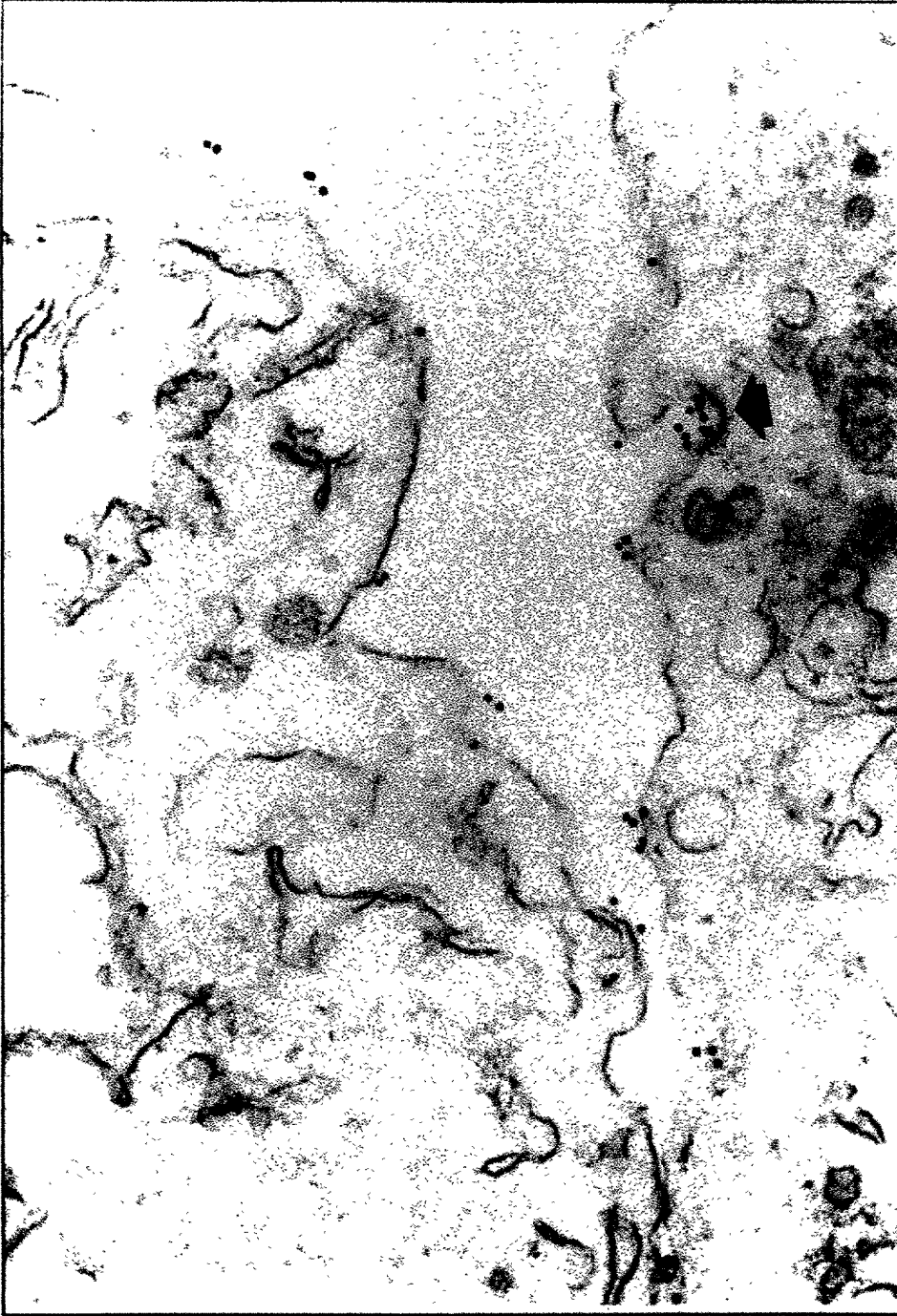


FIG. 2

FIG. 2

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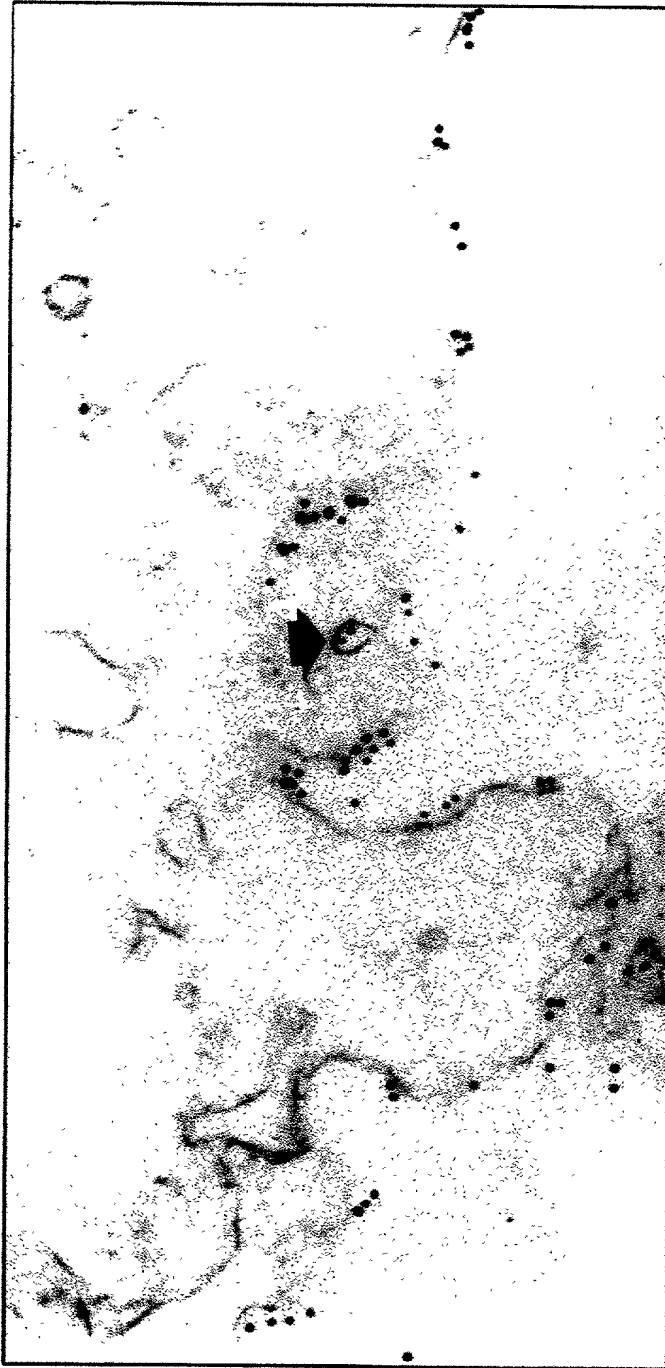


FIG. 3

FIG. 3

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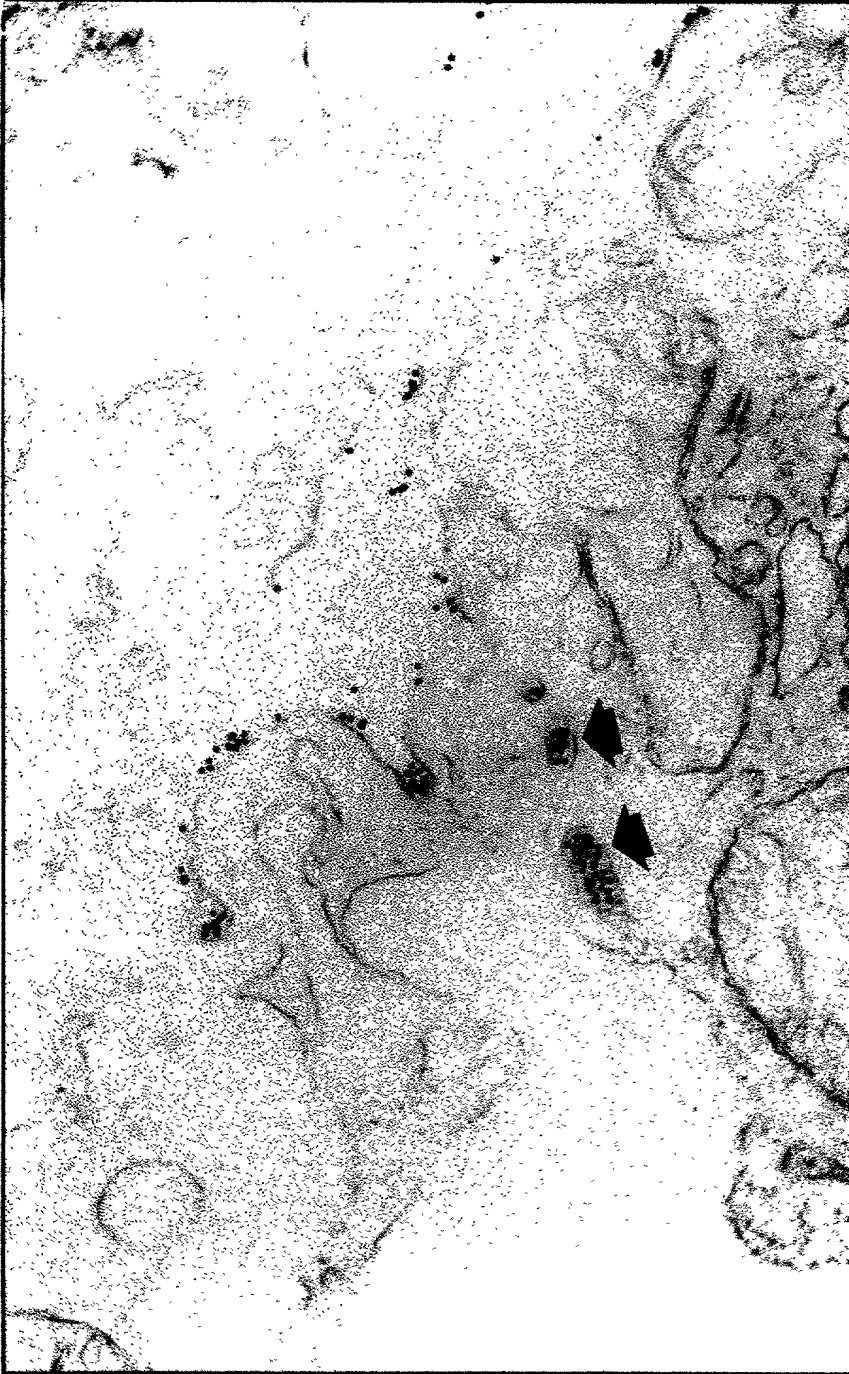


FIG. 4

FIG. 4

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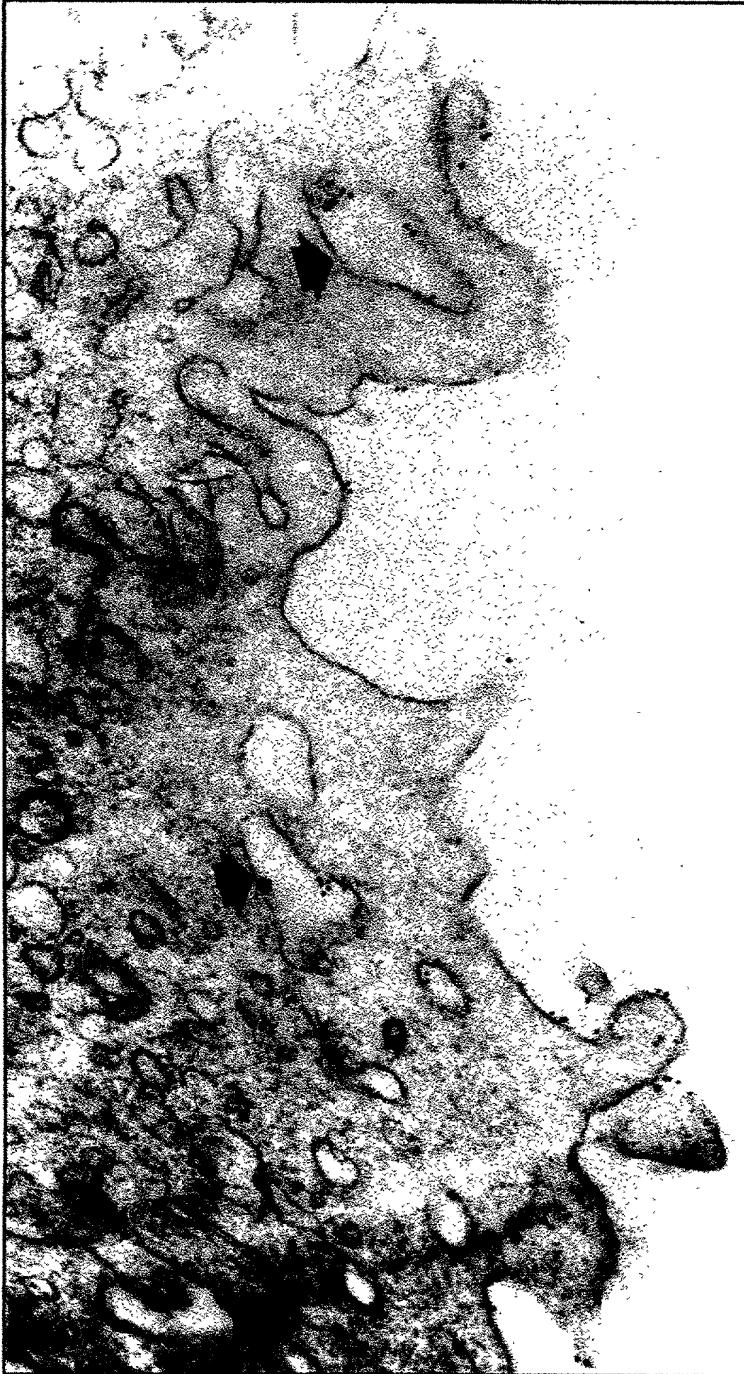


FIG. 5

FIG. 5

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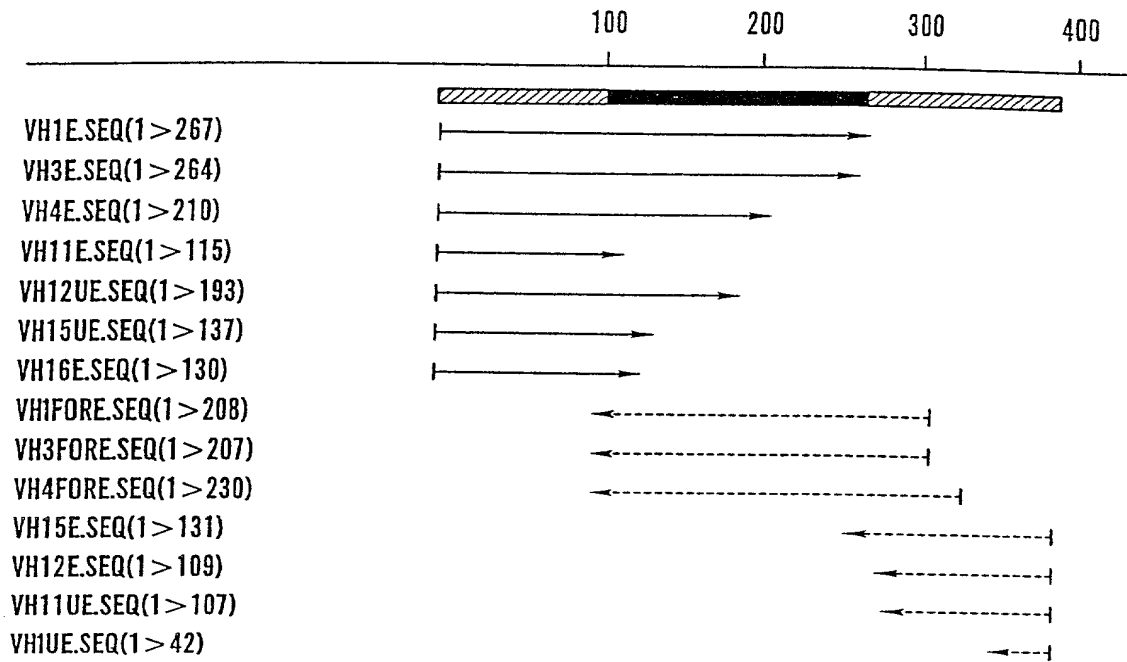


FIG. 6

SN: 09/929,546

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE



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LIPMAN-PEARSON PROTEIN ALIGNMENT
KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115)	SEQ2(1>125)	SIMILARITY	GAP	GAP	CONSENSUS
J591VH.PRO	MUVHIIA.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>115)	(1>125)	75.6	2	10	125

```

      10      20      30      40      50
      ↓      ↓      ↓      ↓      ↓
EVQLQQSGPELVKPGTSVRISCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGGIT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFY:Y: :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFIDYMNWVKQSPGKSLEWIGDINPGNGGTS
      ↑      ↑      ↑      ↑      ↑      ↑
      10      20      30      40      50      60
      ↓      ↓      ↓      ↓      ↓      ↓
YNQKFEDKATLIVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGGIT
YNQKF.:KATLIVDKSSSTAYM:L.SLTSEDSAVYYCA G      ..FDYWGGIT
YNQKFKGKATLIVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSYMAYYAFDYWGQGIT
      ↑      ↑      ↑      ↑      ↑      ↑
      70      80      90      100     110     120

```

LTVSS
:TVSS
VIVSS

FIG. 8

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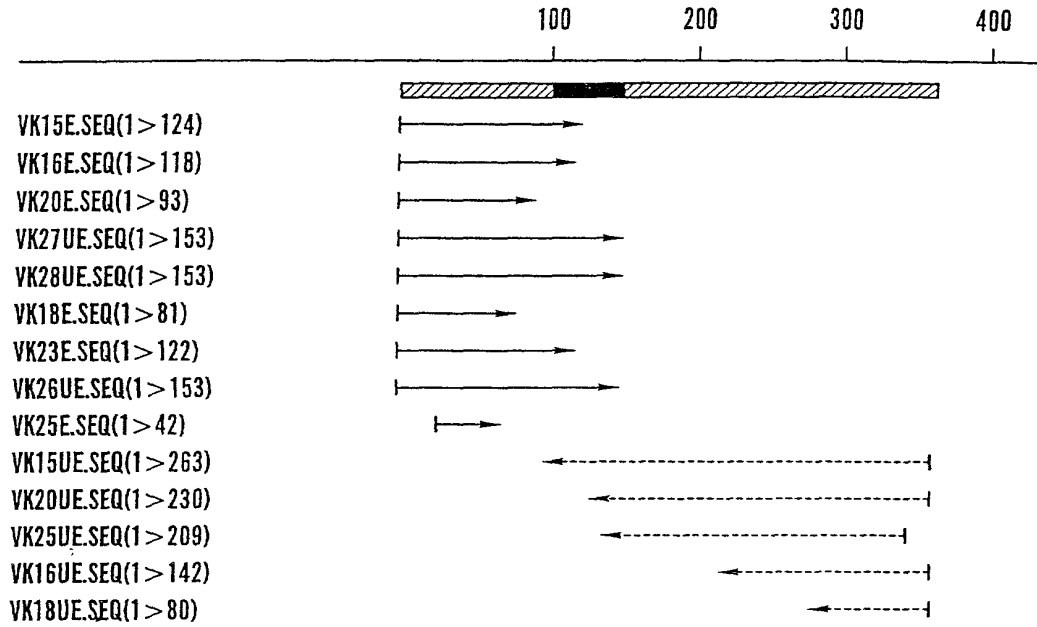


FIG. 9

TREATMENT AND DIAGNOSIS OF CANCER

INV: N. BANDER

SN: 09/929,546

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ENZYMES: ALL 74 ENZYMES (NO FILTER):
 SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

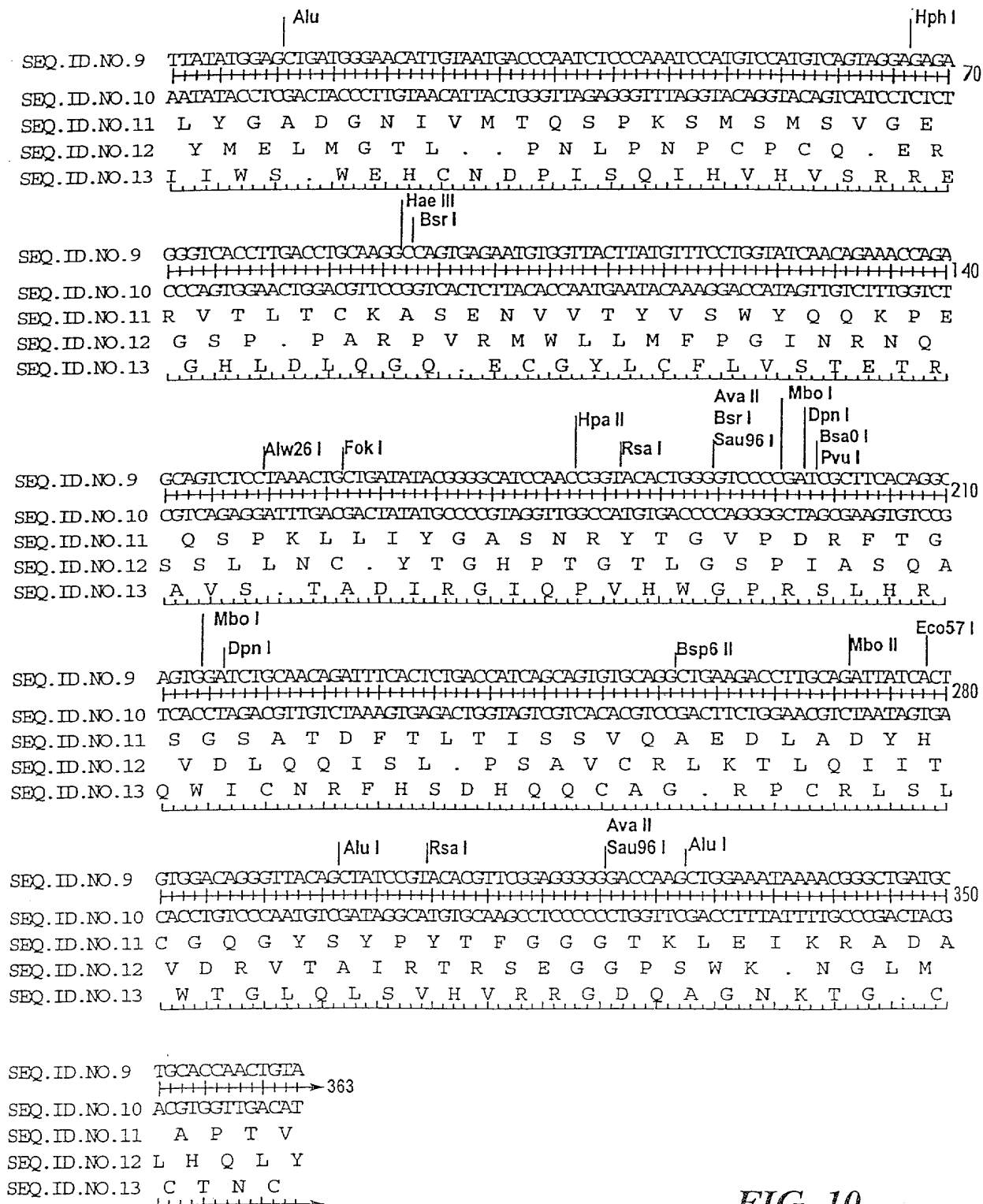


FIG. 10

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LIPMAN-PEARSON PROTEIN ALIGNMENT
KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107) J591VK.PRO	SEQ2(1 > 1 1 1) MUVKV.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>107)	(1>109)	60.4	2	2	109

↓10 ↓20 ↓30 ↓40 ↓50
 NIVMTQSPKSMSSVGERVILTCKAS-ENVVTYVSWYQOKPEQSPKLLIYGASNRYTGVP
 :I MTQSP.S:S S:G:RVT:TC:AS ::: .Y::WYQOKP. SPKLLIY AS. .:GVP
 DIQMTQSPSSLSASLGDRVTITCRASQDDISNYLNNWYQOKPGGSPKLLIYYASRLHSGVP
 ↑10 ↑20 ↑30 ↑40 ↑50 ↑60
 ↓60 ↓70 ↓80 ↓90 ↓100
 DRFTGSGSATDFLTITSSVQAEDLADYHCGQGYSY-PYTFGGGKLEIK
 .RF:GSGS:TD::LTIS:::ED:A.Y C QG : P TFGGKLEIK
 SRFSGSGSGTDYSLTISNLEQEDLATYFCQQGNILPPRTFGGKLEIK
 ↑70 ↑80 ↑90 ↑100

FIG. 11

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